Replace the paragraph beginning at page 8, line 8, with the following rewritten paragraph:

--In further embodiment the conserved peptide motifs as identified comprise:

1. AAQSIGEPGTQLT (SEQ ID NO:1)
2. AGDGTTTAT (SEQ ID NO:2)
3. AGRHGNKG (SEQ ID NO:3)
4. AHIDAGKTTT (SEQ ID NO:4)
5. CPIETPEG (SEQ ID NO:5)
6. DEPSIGLH (SEQ ID NO:6)
7. DEPTSALD (SEQ ID NO:7)
8. DEPTTALDVT (SEQ ID NO:8)
9. DHAGIATQ (SEQ ID NO:9)
10. DHPHGGGEG (SEQ ID NO:10)
11. DLGGGTFD (SEQ ID NO:11)
12. DVLDTWFSS (SEQ ID NO:12)
13. ERERGITI (SEQ ID NO:13)
14. ERGITITSAAT (SEQ ID NO:14)
15. ESRRIDNQLRGR (SEQ ID NO:15)
16. FSGGQRQR (SEQ ID NO:16)
17. GEPGVGKTA (SEQ ID NO:17)
18. GFDYLRDN (SEQ ID NO:18)
19. GHNLQEHS (SEQ ID NO:19)
20. GIDLGTTNS (SEQ ID NO:20)
21. GINLLREGLD (SEQ ID NO:21)
22. GIVGLPNVGKS (SEQ ID NO:22)
23. GKSSLLNA (SEQ ID NO:23)
24. GLTGRKIIVDTYG (SEQ ID NO:24)
25. GPPGTGKTLLA (SEQ ID NO:25)
26. GPPGVGKT (SEQ ID NO:26)
27. GSGKTTLL (SEQ ID NO:27)
28. GTRIFGPV (SEQ ID NO:28)
29. IDTPGHVDFT (SEQ ID NO:29)
30. IIAHIDHGKSTL (SEQ ID NO:30)
31. INGFGRIGR (SEQ ID NO:31)
32. IREGGRTVG (SEQ ID NO:32)
33. IVGESGSGKS (SEQ ID NO:33)
34. KFSTYATWWI (SEQ ID NO:34)
35. KMSKSKGN (SEQ ID NO:35)
36. KMSKSLGN (SEQ ID NO:36)
37. KNMITGAAQMDGAILVV (SEQ ID NO:37)
38. KPNSALRK (SEQ ID NO:38)
39. LFGGAGVGKTV (SEQ ID NO:39)
40. LGPSGCGK (SEQ ID NO:40)
41. LHAGGKFD (SEQ ID NO:41)
42. LIDEARTPLIISG (SEQ ID NO:42)
43. LLNRAPTLH (SEQ ID NO:43)
44. LPDKAIDLIDE (SEQ ID NO:44)
45. LPGKLADS (SEQ ID NO:45)
46. LSGGQQQR (SEQ ID NO:46)
47. MGHVDHGKT (SEQ ID NO:47)
48. NADFDGDQMAVH (SEQ ID NO:48)
49. NGAGKSTL (SEQ ID NO:49)
50. NLLGKRVD (SEQ ID NO:50)
51. NTDAEGRL (SEQ ID NO:51)
52. PSAVGYQPTLA (SEQ ID NO:52)
53. QRVAIARA (SEQ ID NO:53)
54. QRYKGLGEM (SEQ ID NO:54)
55. RDGLKPVHRR (SEQ ID NO:55)
56. SALDVSIQA (SEQ ID NO:56)
57. SGGLHGVG (SEQ ID NO:57)
58. SGSGKSSL (SEQ ID NO:58)
59. SGSGKSTL (SEQ ID NO:59)
60. SVFAGVGERTREGND (SEQ ID NO:60)
61. TGRTHQIRVH (SEQ ID NO:61)
62. TGVSGSGKS (SEQ ID NO:62)
63. TLSGGEAQRI (SEQ ID NO:63)
64. TNKYAEGYP (SEQ ID NO:64)
65. TPRSNPATY (SEQ ID NO:65)
66. VEGDSAGG (SEQ ID NO:66)
67. VRKRPGMYIG (SEQ ID NO:67)--

Replace the paragraph beginning at page 12, line 23, with the following rewritten paragraph:

--Figure 4 shows crystal structures of three invariant peptides (**VRKRPGMYIG** (SEQ ID NO:67), **LHAGGKFD** (SEQ ID NO:41) and **SGGLHGVG** (SEQ ID NO:57)) from DNA gyrase B protein.--

Replace the paragraph beginning at page 13, line 22, with the following rewritten paragraph:

--Downloaded Files and their format:

<organism_name>. pep : file which stores the annotation & the protein sequence

<organism-name> refers to

Tb (*Mycobacterium tuberculosis*) **Bs** (*Bacillus subtilis*) **Mg** (*Mycoplasma genitalium*) **Mp** (*Mycoplasma pneumonoa*) **Ec** (*Escherichia coli*) **Hp** (*Helicobacter pylori*) **Hi** (*Haemophilus influenzae*)

Format: FASTA

">gi|"<annotation>
<<the entire protein sequence.....

For example,

>gi|2808711|emb|CAA16238.1|dnaA
MTDDPGSGFTTVWNAVVSELNGDPKVDDGPSSDANLSAPLTPQQRAWLNLVQPLTIVE
GFALLSVPSSFVQNEIERHLRAPITDALSRRLGHQIQLGVRIAPPATDEADDTTVPPSENP
ATTSPDTTDNDEIDDSAAARGDNQHSWP.....(SEQ ID NO:68)

>gi|3261513|emb|CAA16239.1|dnaN
MDAATTRVGLTDLTFRLLRESFADAVSWVAKNLPARPAVPVLSGVLLTGSDNGLTISGF
DYEVSAEAQVGAEIVSPGSVLVSGRLLSDITRALPNKPVDVHVEGNRVALTCGNARFSL
PTMPVEDYPTLPTLPEETGLLPAE.....(SEQ ID NO:69)--

Replace the paragraph beginning at page 15, line 17, with the following rewritten paragraph:

--An invariant peptide having sequence **FSGGQRQR** (SEQ ID NO:16) was found to exist in oppF/dppF proteins of six organisms out of the seven examined (except for in *M. tuberculosis*). This protein functions as an ATP binding protein. Since this invariant peptide has also been found to be located on the hypothetical protein encoded by **Rv1273c** gene in *M. tuberculosis*, it is suggested that this protein encoded by **Rv1273c** gene must function as ATP binding protein as it holds the signature of this class of protein.--

a5

Replace the paragraph beginning at page 15, line 25, with the following rewritten paragraph:

--Another invariant peptide having sequence **GIVGLPNVGKS** (SEQ ID NO:22) was found in proteins having GTP binding function in six bacteria out of the seven examined (except for in *M. tuberculosis*) where as the same invariant sequence is present in hypothetical protein encoded by **Rv1112** protein in *M. tuberculosis*. It is strongly suggested that this hypothetical protein may have GTP binding property as it holds the signature of this class of protein.--

a6

Replace the paragraph beginning at page 16, line 3, with the following rewritten paragraph:

--Enzyme DNA gyrase is known to reduce supercoiling of DNA. This protein is absent in human and has been considered as a potential drug target. However, the exact sequence to which the drug molecules should be targeted is not yet clear. The peptides such as **VRKRPGMYIG** (SEQ ID NO:67), **LHAGGKFD** (SEQ ID NO:41), **SGGLHGVG** (SEQ ID NO:57), **LPGKLADC** (SEQ ID NO:45), **VEGDSAGG** (SEQ ID NO:66) and **QRYKGLGEM** (SEQ ID NO:54) that are invariant across many pathogenic and non-pathogenic bacterial DNA gyrase beta subunit, but absent in host, are the structural determinants which could be used as potential drug targets against bacterial infections. The crystal structures of three of these peptides are shown in fig 4.--

a7